

REMARKS

Claim Rejections – 35 USC §101

Claims 1 to 3 have been rejected as being directed to non-statutory subject matter.

Claims 1 to 3 have been amended to include the appropriate language to obviate this rejection. Withdrawal of this rejection is respectfully requested.

Claim Rejections – 35 USC §112

Claims 1 to 9 have been rejected as not being non-enabled by the specification.

Independent claims 1 and 2 have been amended to claim SEQ ID NO. 1 and the DNA of SEQ ID NO. 1 as follows:

1. (Currently Amended) An isolated protein comprising:
an amino acid sequence represented by SEQ ID NO: 1.
2. (Currently Amended) An isolated DNA encoding a protein
comprising:
an amino acid sequence represented by SEQ ID NO: 1.

Thus, claims 1 and 2 as amended and their dependent claims (claims 3 to 9) are supported and fully enabled by the specification. Withdrawal of this rejection is respectfully requested.

Claim Rejections – 35 USC §102

Claims 1 to 3 have been rejected as being anticipated by Bonin et al. (Plant Physiol., Vol. 114(3), Sup. page 22, Abstract 20). Claims 1 to 2 and 4 to 8 have been rejected as being anticipated by Andrianopoulos et al. (J. Bacteriol., Vol. 180(4): 998-1001).

With respect to Bonin et al., the Examiner takes the position that the enzyme identified in Bonin et al. is the same as SEQ ID NO. 1 of the present application even though, Bonin et al. does not disclose the actual amino acid sequence or the polynucleotide sequence. Applicants disagree with this assumption for the following reasons.

The amino acid sequence of GER1 was registered with GenBank by Bonin et al. under the accession number AAC02703 on February 12, 1998. Enclosed is a copy of GenBank registered information (Exhibit 1). Therefore, it is validly assumed that the protein having the amino acid sequence registered with GenBank corresponds to the GER1 protein of Bonin et al.

A comparison was made between the amino acid sequence of the AtFX1 protein (SEQ ID NO: 1) and the registered amino acids sequence of GER1 protein of Bonin et al. As a result, it is revealed that they have 93.7% homology in amino acids. Bonin's et al.'s GER1 protein is shown to have eighteen differences in amino acids (including a contiguous difference of sixteen amino acids), one deletion of an amino acid, and three insertions of amino acids when compared to the AtFX1 protein. A copy of the result of the comparison is enclosed as Exhibit 2.

Therefore, it is submitted that the protein of claim 1 as amended is different from the GER1 protein of Bonin et al.

When comparing the amino acid sequence and nucleotide sequence of the claimed protein (AtFX1) with the protein disclosed in Andrianopoulos et al. (WcaG), it can be noted that they have only 56.3% homology in amino acids and 58.2% homology in nucleotides. Copies of the comparison results are enclosed as Exhibits 3 and 4. Also, the WcaG protein was isolated from *E. coli.*, whereas the AtFX1 protein was isolated from *Arabidopsis*.

Therefore, the protein of claim 1 is different from the WcaG protein of Andrianopoulos et al.

Thus, both Bonin et al. and Andrianopoulos et al. do not anticipate the presently claimed invention as set forth in claims 1 to 8 at least for the above reasons.

Applicant : Ken-ichi Nakayama et al.
Serial No. : 10/089,014
Filed : March 25, 2002
Page : 6 of 6

Attorney's Docket No.: 11283-019US1 / PH-935PCT-
US

It is noted that claim 9 has not been rejected on the basis of anticipation. Thus, it is assumed that by overcoming the 112 rejections of the basis claims, claim 9 would be allowable.

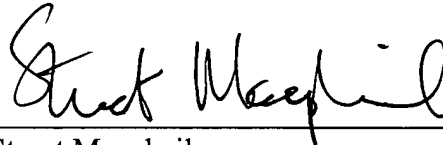
In summary, at least for the foregoing reasons, Applicants submit that all of the claims have overcome the rejections set forth. It is respectfully requested that all pending claims be allowed.

Enclosed is a check for the Petition for Extension of Time fee (one-month). Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

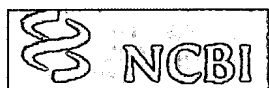
Date: _____

10/9/03



Stuart Macphail
Reg. No. 44,217

Fish & Richardson P.C.
45 Rockefeller Plaza, Suite 2800
New York, New York 10111
Telephone: (212) 765-5070
Facsimile: (212) 258-2291

Document |
GenBank information

PubMed Nucleotide Protein Genome Structure PDB Taxonomy OMIM

Search for

Display Limits Preview/Index History Clipboard De

1: AAC02703[gi:2865623] This record was replaced or removed. See revision history for details.

LOCUS AAC02703 314 aa linear PLN 12-FEB-1998
DEFINITION GDP-4-keto-6-deoxy-D-mannose-3, 5-epimerase-4-reductase [Arabidopsis thaliana].
ACCESSION AAC02703
VERSION AAC02703.1 GI:2865623
DBSOURCE locus AF045286 accession AF045286.1
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (residues 1 to 314)
AUTHORS Bonin, C. P., Potter, I., Vanzin, G. F. and Reiter, W. -D.
TITLE A bifunctional epimerase-reductase completes the de novo synthesis of GDP-L-fucose in Arabidopsis
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 314)
AUTHORS Bonin, C. P., Potter, I., Vanzin, G. F. and Reiter, W. -D.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1998) Molecular and Cell Biology, University of Connecticut, 75 North Eagleville Road, Storrs, CT 06269, USA
COMMENT [WARNING] On Oct 8, 1999 this sequence was replaced by a newer version gi:6016479.
Method: conceptual translation supplied by author.
FEATURES
source Location/Qualifiers
1..314
/organism="Arabidopsis thaliana"
/cultivar="Columbia ecotype"
/db_xref="taxon:3702"
Protein 1..314
/product="GDP-4-keto-6-deoxy-D-mannose-3, 5-epimerase-4-reductase"
/name="enzyme in pathway for de novo synthesis of GDP-L-fucose"
CDS 1..314
/gene="GER1"
/coded_by="AF045286.1:49..993"
ORIGIN
1 msdksakifv aghrglvgsa ivrklqeqgf tnlvklthae ldltqadve sffsqekpvy
61 vilaaakvgg ihanntypad figvnlqiot nvihsayehg vkklflgss ciypkfapqp
121 ipesalltas leptnewyai akiagiktco ayriqhgwda isgmptnlyg pndnfhpesh
181 vlpalmrffh eakvnwsggs cgvgkvvpl egkflhvddl adacvflldr iqrglehnvi
241 gsgqevtire laelvkevvg fegklgdct kpdgtprklm dssklaslgw tpkvsldrgl
301 satydwylnk vcnr

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Seq. ID 2865623.12.15.10

[GENETYX-MAC : Amino Acid Sequence Homology Data]

Date : 2003.08.18

1st Amino Acid Sequence

File Name : Gerlp.ptn
Sequence Size : 314

2nd Amino Acid Sequence

File Name : AtFX1.ptn
Sequence Size : 312

Unit Size to compare = 2

Pick up Location = 2

[93.7% / 315 aa]

INT/OPT. Score : < 869/ 1415 >

```
1' MSDKSAKIFVAGHRGLVGS AIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFS QEKPVY
*****
1" MSDKSAKIFVAGHRGLVGS AIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFS QEKPVY

61' VILAAAKVGGIHANN TYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
*****
61" VILAAAKVGGIHANN TYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP

121' IPESALLTASLEPTNEWY AIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPE-S
*****
121" IPESALLTASLEPTNEWY AIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS

180' HVLPALMRRFHEAKVN WSGGSCGVGYKVVPLEGKFLHVDDLADACVFLLDRIQRGLEHVN
*****
181" HVLPALMRRFHEAKVN --GAEEVVVWGTGSPLREFLHVDDLADACVFLLDRI--SGLEHVN

240' IGSQGEVTIRELAELVKEVVGFEGLGWDCTKPDGTPRKLMDSKSLASLGWTPKVS LRDG
*****
238" IGSQGEVTIRELAELVKEVVGFEGLGWDCTKPDGTPRKLMDSKSLASLGWTPKVS LRDG

300' LSQTYDWYLKNVCNR
*****
298" LSQTYDWYLKNVCNR
```

[93.7% / 315 aa]

INT/OPT. Score : < 425/ 1415 >

```
1' MSDKSAKIFVAGHRGLVGS AIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFS QEKPVY
*****
1" MSDKSAKIFVAGHRGLVGS AIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFS QEKPVY

61' VILAAAKVGGIHANN TYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
*****
61" VILAAAKVGGIHANN TYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP

121' IPESALLTASLEPTNEWY AIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPE-S
*****
121" IPESALLTASLEPTNEWY AIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS
```

180' HVLPALMRRFHEAKVNWSGGSCGVGYKVPLEKFLHVDDLADACVFLLDRIQRGLEHVN
***** * . . * . . . *****
181" HVLPALMRRFHEAKVN--GAEEVVVWGTGSPLREFLHVDDLADACVFLLDRI--SGLEHVN
240' IGSGQEVTI RELAE LVKEVVGFEGLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG

238" IGSGQEVTI RELAE LVKEVVGFEGLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG
300' LSQTYDWYLKNVCNR

298" LSQTYDWYLKNVCNR

[GENETYX-MAC : Amino Acid Sequence Homology Data]

Date : 2003.08.18

1st Amino Acid Sequence

File Name : AtFX1.ptn
Sequence Size : 312

2nd Amino Acid Sequence

File Name : wcaG.ptn
Sequence Size : 321

Unit Size to compare = 2

Pick up Location = 2

[56.3% / 311 aa]

INT/OPT.Score : < 565/ 918 >

```

1' MSDKSAKIFVAGHRGLVGS AIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFS QEKPVY
   ..*,*****,* *..* ..*,*..* * ..*,*..*
1"  MSKQRVFIAGHRGMVGS AIRRQLEQRGDVELVLRTRDELNLLDSRAVHDF FASERIDQ

61' VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
   * ***** * ..*,*..* * ..*,*..* * ..*,*..* * ..*,*..*
59" VYLAAAKVGGIVANNTYPADFIYQNMIESNI IHAHQNDVNKLLFLGSSCIYPKLAKQP

121' IPESALLTASLEPTNEWYAI AKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS
   ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..*
119" MAESSELLQGTLEPTNEPYAI AKIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPNS

181' HVLPALMRRFHEAKVNGAEV VVWGTGSPLREFLHVDDLADACVFL-----DRYS
   ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..*
179" HVIPALLRRFHEATAQNAPD VVWVGSGTPMREFLHVDDMAAAS IHVMELAHEVWLENTQP

232' GLEHVNIGSGQEV TIRELAELVKEVVGFEGLGWDCTKPDGTPRKLMDSKSLASLGWTPK
   ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..*
239" MLSHINVGTGV DCTIRDVAQTI AKVVG YKGRVVF DASKPDGTPRKLLDVTRLHQLGWYHE

292' VSLRDGLSQT YDWYLNVCNR
   ..*,*..* ..*,*..*
299" ISLEAGLASTYQWFLENQDRFRG

```

[56.3% / 311 aa]

INT/OPT.Score : < 121/ 918 >

```

1' MSDKSAKIFVAGHRGLVGS AIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFS QEKPVY
   ..*,*****,* *..* ..*,*..* * ..*,*..*
1"  MSKQRVFIAGHRGMVGS AIRRQLEQRGDVELVLRTRDELNLLDSRAVHDF FASERIDQ

61' VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
   * ***** * ..*,*..* * ..*,*..* * ..*,*..* * ..*,*..*
59" VYLAAAKVGGIVANNTYPADFIYQNMIESNI IHAHQNDVNKLLFLGSSCIYPKLAKQP

121' IPESALLTASLEPTNEWYAI AKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS
   ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..* ..*,*..*
119" MAESSELLQGTLEPTNEPYAI AKIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPNS

```

181' HVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLL-----DRYS
 .*.*****.***.*****.***.*****.***.***.
 179" HVIPALLRRFHEATAQNAPDVVWVGSGTPMREFLHVDDMAAASIHVMELAHEVWLENTQP
 232' GLEHVNIGSGQEVITIRELAELVKEVVGFEGLGWDCTKPDGTPRKLMDSSKLASLGWTPK
 *.***.***.***.***.***.***.***.***.***.***.***.
 239" MLSHINVTGVDCTIRDVAQTIKVVGYKGRVVFDAKPDGTPRKLLDVTRLHQLGWYHE
 292' VSLRDGLSQTYDWYLNVCNR
 .*.***.***.***.
 299" ISLEAGLASTYQWFLENQDRFRG

[GENETYX-MAC : Nucleotide Sequence Homology Data]

Date : 2003.08.18

1st Nucleotide Sequence

File Name : AtFXorf.nuc
Sequence Size : 939

2nd Nucleotide Sequence

File Name : wcaG.nuc
Sequence Size : 966

Unit Size to Compare = 4

Pick up Location = 2

[58.2% / 933 bp] INT/OPT.Score : < 1084/ 1266 >

```
1' ATGTCTGACAAATCTGCCAAATCTTCGTCGCGGGTCATCGTGGTTGGTTGGATCTGCC
   * * * * *
1"  ATGAGTAAACAACGAGTTTTATTGCTGGTCATCGCGGGATGGTCGGTTCCGCC

61' ATTGTCCGCAAGCTTCAGGAACAAGTTTCACCAATCTCGTTCTTAAACACACGCCGAG
   ** ** * * * * *
55" ATCAGGCGGCAGCTCGAACAGCGCGGTGATGTGGAACGGTATTACGCACCCGCGACGAG

121' CTTGATCTCACTCGTCAAGC-CGATGTTGAATCCTTCTTTCTCAAGAGAAGCCAGTTTA
   * * * * *
115" C-TGAACCTGCTGGACAGCCGCCGTGCATGATTCTTTGCCAGCGAACGTATTGACCA

180' TGTAATCCTAGCAGCAGCTAAAGTTGGTGGTATTACGCTAACAACACCTATCCTGCTGA
   ** ** * * * * *
174" GGTCTATCTGGCGGCGGCAAGTGGGCGGCATTGTTGCCAACAACACCTATCCGGCGGA

240' TTTCAATGGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGG
   *****
234" TTTCACTACCAGAACATGATGATTGAGAGCAACATCATTACGCCCGCGCATCAGAACGA

300' TGTGAAGAAGCTTCTCTCTTGGATCATCCTGCATTACCTAAATTTGCTCCTCAGCC
   *****
294" CGTGAACAAACTGCTGTTTCTCGGATCGTCCTGCATCTACCCGAAACTGGCAAAACAGCC

360' AATTCCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTAT
   ** * * *
354" GATGGCAGAAAGCGAGTTGTTGAGGGCACGCTGGAGCCGACTAACGAGCCTTATGCTAT

420' TGCTAAGATCGCTGGGATTAAGACTTGTGAGGCTTATAGGATTCAGCACGGATGGGATGC
   *** **
414" TGCCAAATCGCCGGGATCAAAGTGTGCGAATCATACAACGCCAGTACGGACGCGATTA

480' AATCTCTGGCATGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGAGAATTC
   *** *
474" CCGCTCAGTCATGCCGACCAACCTGTACGGGCCACACGACAACTTCCACCCGAGTAATTC

540' TCATGTGCTTCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGA
   *****
534" GCATGTGATCCCAGCATTGCTGCGTCGCTTCCACGAGGCGACGGCACAGAATGCGCCGGA
```

600' AGTTGTGGTGTGGGGTACAGGTAGTCCGTTGAGGGAGTTCTTGCATGTTGATGATTGG-
 ** ***** ** ***** ** ***** ** ***** ** ***** **
 594" CGTGGTGGTATGGGGCAGCGGTACACCGATGCGCGAATTTCTGCACGTCGATGATATGGC
 659' -----CTGATGCT----TGTGTTTTCTTGCTGGA-TCGATACAGCG
 ** *** ** *** ***** * *****
 654" GCGCGCGAGCATTTCATGTCATGGAGCTGGCGCATGAAGTCTGGCTGGAGAACACCCAGCC
 695' GGT--TGGAGCATGTAAACATTGGAAGTGGTCAAGAAGTGAAGTATTAGAGAGTTGGCTGA
 * * ** ***** * * * * * ** ***** * * * * *
 714" GATGTTGTCGCACATTAACGTCGGCAGGGCGTTGACTGCACTATCCGCGACGTGGCGCA
 753' GTTGGTGAAAGAGGTTGTTGGTTTTGAAGGGAAGCTTGGATGGGATTGCACTAAGCCAGA
 * * * * * ***** ***** * * * * * ** *****
 774" AACCATCGCCAAAGTGGTGGGTTACAAAGGCCGGGTGGTTTTTGTATGCCAGCAAACCGGA
 813' TGGCACACCGAGGAACTTATGGACAGCTCAAAGCTCGCGTC-TTGGGTTGGACACCTA
 ***** ** * ***** ***** * ** * * * * * * * * *
 834" TGGCAGCGCGCGCAAACCTGCTGGA-TGTGACGCGCCTGCATCAGCTTGGCTGGTATCACG
 872' AGGTTTCTCTTAGAGATGGTCTGAGCCAACTTATGATTGGTATTGAAGAATGTTTGCA
 * * * * * ** * * * * * * ***** * ***** * *****
 893" AAATCTCACTGGAAGCGGGGCTTGCCAGCACTTACCAGTGGTTCCTTGAGAATCAAGACC
 932' ACCGATAA
 953" GCTTTCGGGGGTAA

[58.2% / 933 bp] INT/OPT. Score : < 262/ 1266 >

1' ATGTCTGACAAATCTGCCAAATCTTCGTCGCGGGTCATCGTGGTTTGGTTGGATCTGCC
 * * * * * ** ***** ** ***** ** *****
 1" ATGAGTAAACAACGAGTTTTTATTGCTGGTCATCGCGGATGGTCCGTTCCGCC
 61' ATTGTCCGAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAACACACGCCGAG
 ** ** ***** * * * * * ** * * * * *
 55" ATCAGGCGGCAGCTCGAACAGCGCGGTGATGTGGAAGTGGTATTACGCACCCGCGACGAG
 121' CTTGATCTCACTCGTCAAGC-CGATGTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTA
 * * * * * ** * * * * * * ***** * * * *
 115" C-TGAACCTGCTGGACAGCCGCGCGTGCATGATTCTTTGCCAGCGAACGTATTGACCA
 180' TGTAATCCTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCTATCCTGCTGA
 ** ** * * * * * ***** ** * * * * * *****
 174" GGTCTATCTGGCGGCGGCGAAAGTGGGCGGCATTGTTGCCAACAACACCTATCCGGCGGA
 240' TTTCATTGGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGG
 ***** ** * ***** ** * * * * * ** * * * * *
 234" TTTCATCTACCAGAACATGATGATTGAGAGCAACATCATTACGCGCGCATCAGAACGA
 300' TGTGAAGAAGCTTCTCTTCTTGGATCATCCTGCATTACCTAAATTTGCTCCTCAGCC
 ***** ** * * * * * ***** ***** ***** * * * * *
 294" CGTGAACAAACTGCTGTTTCTCGGATCGTCCTGCATCTACCCGAAACTGGCAAAACAGCC
 360' AATTCCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTAT
 ** * * * * * ***** * ***** ** * * * * * *****
 354" GATGGCAGAAAGCGAGTTGTTGCAGGGCACGCTGGAGCCGACTAACGAGCCTTATGCTAT

```

420' TGCTAAGATCGCTGGGATTAAGACTTGTGTCAGGCTTATAGGATTCAGCACGGATGGGATGC
*** ** ***** ** ** * * * * * *** ***** * ***
414" TGCCAAAATCGCCGGGATCAAACGTGCGAATCATACAACCGCCAGTACGGACGCGATTA
480' AATCTCTGGCATGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGGAGAATTC
*** * ***** ** ** * * * * * * * ***** *****
474" CCGCTCAGTCATGCCGACCAACCTGTACGGGCCACACGACAATTCCACCCGAGTAATTC
540' TCATGTGCTTCCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGA
***** * * * * * * * * * * * * * * * * * * * * *
534" GCATGTGATCCCAGCATTGCTGCGTCGCTTCCACGAGGCGACGGCACAGAATGCGCCGGA
600' AGTTGTGGTGTGGGTACAGGTAGTCCGTTGAGGGAGTTCTTGCATGTTGATGATTTGG-
** ***** ***** * ***** ** * * * * * ***** ** *****
594" CGTGGTGGTATGGGGCAGCGGTACACCGATGCGCGAATTTCTGCACGTCGATGATATGGC
659' -----CTGATGCT----TGTGTTTCTTGCTGGA-TCGATACAGCG
** ** * * * * * * * * * *
654" GGCGGCGAGCATTTCATGTCATGGAGCTGGCGCATGAAGTCTGGCTGGAGAACACCCAGCC
695' GGT--TGGAGCATGTTAATTTGAAGTGGTCAAGAAGTGAATATTAGAGAGTTGGCTGA
* * * * * ***** * * * * * * * ***** * * * * *
714" GATGTTGTCGCACATTAACGTCGGCACGGGCGTTGACTGCACTATCCGCGACGTGGCGCA
753' GTTGGTGAAGAGGTTGTTGGTTTTGAAGGGAAGCTTGGATGGGATTGCTAAGCCAGA
* * * * * ***** ***** * * * * * * * * * *
774" AACCATCGCCAAAGTGGTGGGTACAAAGGCCGGGTGGTTTTTGATGCCAGCAAACCGGA
813' TGGCACACCGAGGAACTTATGGACAGCTCAAAGCTCGCGTC-TTGGGTTGGACACCTA
***** * * * * * * * * * * * * * * * * * * * *
834" TGGCACGCCGCGCAAACCTGCTGGA-TGTGACGCGCCTGCATCAGCTTGGCTGGTATCAG
872' AGGTTTCTCTTAGAGATGGTCTGAGCCAACTTATGATTGGTATTTGAAGAATGTTTGCA
* * * * * * * * * * * * * * * * * * * *
893" AAATCTCACTGGAAGCGGGGCTTGCCAGCACTTACCAGTGGTTCCTTGAGAATCAAGACC
932' ACCGATAA
953" GCTTTCGGGGGTAA

```

1st Nucleotide Sequence

File Name : AtFXorf.nuc (Complementary)
Sequence Size : 939

2nd Nucleotide Sequence

File Name : wcaG.nuc
Sequence Size : 966

Unit Size to Compare = 4
Pick up Location = 2

[44.7% / 770 bp] INT/OPT.Score : < 58/ 198 >

1' TTATCGGTTGCAAAC-ATTCTTCAAATACCAATCATAAG

```

***** ** * * * * *
181" CTGGCGGCGGCGAAAGTGGGCGGCATTGTTGCCAACAACACCTATCCGGCGGAT-TTCAT
39' TTTGGCTCAGACCATCTCTAAGAGAAACCTTAGGTGTCCAACCCAAAGACGCGAGCTTTG
* * * * *
240" CTACCAGAACATGATGATTGAGAGCAACATCA----TTCACGCCGCGCATCAGAACGACG
99' AGCTGTCCATAAGTTTCCTCGGTGTGCCATCTGGCTTAGTGCAATCCCATCCAAGCTTCC
* * * * *
296" TGAACAAACTGCTGTTTCTCGGATCGTC--CTGCATCTACCCGAAACTGGCAAAACAGCC
159' CTTCAAAACCAACAACCTCTTTCA-CCAACTCAGCCAACCTCTCTAATAGTCACTTCTTGA
* * * * *
354" GATGGCAGAAAGCGAGTTGTTGCAGGGCAGCTG-GAGCCGACTAA-CGAGCCTT-ATG-
218' CCACTTCCAATGTTAACATGCTCCAACCCGCTGTATCGATCCA--GCAAGAAAACACAAG
* * * * *
410" CTATTGCCAAAATCGCCGGGATCAAACCTGTGCGAATCATAAACC GCCAGTACGGACGCG
276' CAT-CAGCCAAATCAT--CAACATGCAAGAACTCCCTCAACGGACTACCTGTACCCCA--
* * * * *
470" ATTACCGCTCAGTCATGCCGACCAACCTGTACGGGC-CACACGACAACTTCCACCCGAGT
331' CACCACAACCTTCTCCGCTCCATTCACTTTCG---CCTCGTGGAACCTCCTCATAA-GAG
* * * * *
529" AATTCGCATGTGATCCCAGCATTGCTGCGTCGCTTCCACGAGGCGACGGCACAGAATGCG
387' CAGGAAGCACATGAGAATTCTCCG-GGTGGA---AATTGTCATTAGGACCATAGAGATTA
* * * * *
589" CCGGACG-TGGTGGTATGGGGCAGCGGTACACCGATGCGCGAATTTCTGCACGTCGATGA
443' GTAGGCATGCCAGAGATTGCATCCCATCCGTGCTGAATCCTATAAGCCTGACAAGTCTTA
*** * * * *
648" TATGGCGGCGGCGAGCATTATGTCAT-GGAGCTGGCGCAT-GAAGTCTGGCTGGAGAAC
503' ATCCCAGCGATCTT--AGCA-ATAGCATACCACTCATTAGTTGGTTCAAGCGATGCTGTT
* * * * *
706" ACCCAGCCGATGTTGTGCGACATTAACGTCGGCAGGGCGGTTGACTGCA-CTATCCGCGA
560' AACAAAGCAGA--CTCAGGAATTGGCTGAGGAGCAAATTTAGGGTAAATGCAGGATGATC
*** * * * *
765" CGTGGCGCAAACCATCGCCAAAGTGGTGGGTTACAAAGGCCGGGTGGTTTTTGATGCCAG
618' CAAGGAAGAGAAGCTTCTTCACACCGTGCT-CATATGCAGAG--TGGATCACATTGGTCT
*** ** * * *
825" CAAACCGGATGGCAGCGCGCAAACCTGCTGGATGTGACGCGCCTGCATCAGCTTGGCTG
675' GAATCTGGAGAT-TGACACCAA--TGAAATCAGCAGGA--TAGGTGTTGTTAGCGTGAAT
* * * * *
885" GTATCACGAAATCTCACTGGAAGCGGGGCTTGCCAGCACTTACCAGTGGTT-CCTTGAGA
730' ACCACCAACTTTAGCTGCTGCTAGGATTACATAAACTGGCTTCTCTTGAGAAAAGAAGGA
* * * * *
944" ATCAAGACCGCTTTCGGGGGTAA

```

[46.6% / 163 bp] INT/OPT. Score : < 44/ 64 >

721' AGCGTGAATACCACCAACTTTAGCTGCTGCTAGGATTACATAAACTGGCTTCTCTTGAGA

1" ****
ATGAGT

781' AAAGAAGGA--TTCAACATCGGCTTGACGAGTGA-GATCAAGCTCGGCGTGTGTTTAAG
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7" AAACAACGAGTTTTTATTGCTGGTCATCGCGGATGGTCGGTTCCGCCATCAGGCGGCAG

838' AACGAGATTGGTGAAACCTTGTTCTGAAGCTTGCGGACAATGGCAGATCCAACCAAACC
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67" CTCGAACAGCGCGGTGATGTGGAACGTG-TATTACGCAC--CCGC-GA-CGAGCTGAACC

898' ACGATGACCCGCGACGAAGATTTGGCAGATTTGTCAGACAT
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122" TGCTGGA-CAGCCGCGCGTGCATGATTTCTTTGCCAGCGAACGTATTGACCAGGTCTAT